Please amend claims 1, 2, 3, 5-9, 11, and 12 and add new claims 16 – 18 as follows:

1.   (Currently Amended) A method for assembling nucleic acid base sequences comprising the steps of:

providing a plurality of nucleic acid base sequences;

moving an <u>alignment</u> window of a fixed <u>base</u> length along a first nucleic acid base sequence of the plurality of nucleic acid base sequences to define a first fixed-length sequence and simultaneously searching for a second nucleic acid base sequence ~~among the plurality of nucleic acid base sequences which has~~ <u>having a</u> <u>terminal region matching exactly with the window of fixed base length;</u> ~~a second~~ ~~fixed-length partial sequence at a terminal region thereof exactly matching with the~~ ~~first fixed-length partial sequence defined by the window;~~

determining whether the second nucleic acid base sequence ~~searched in said~~ ~~moving step~~ and the first nucleic acid base sequence can be assembled or not by comparing a sequence adjacent to the <u>aligned window of</u> said first ~~fixed-length~~ <u>nucleic acid base</u> sequence ~~of said first nucleic acid base sequence~~ with a sequence adjacent to the <u>aligned window</u> of said second ~~fixed-length~~ <u>nucleic acid base</u> sequence ~~of the second nucleic acid base sequence to be sufficiently similar via a high-speed~~ ~~algorithm~~; and

assembling said first nucleic acid base sequence and said second nucleic acid base sequence ~~if the second nucleic acid base sequence and the first nucleic acid base~~ ~~sequence are determined to be assembled~~ <u>if the sequences adjacent to the aligned</u> <u>windows are similar.</u>

2.   (Previously Presented) A method for assembling nucleic acid base sequences according to claim 1, wherein the nucleic acid base sequence assembled in said assembling step is used as a reconstructed first nucleic acid base sequence to repeatedly carry out said moving, determining, and assembling steps.

3.   (Currently Amended) A method for assembling nucleic acid sequences comprising the steps of:

providing a plurality of nucleic acid base sequences;

entering identification information of each of the plurality of nucleic

acid base sequences ~~and a~~ and the respective fixed base length ~~partial~~ sequence located in a terminal region of each of the nucleic acid base sequences into a table;

constructing a first consensus sequence based on a first nucleic acid base sequence of the plurality of nucleic acid base sequences;

searching the table for a second nucleic acid base sequence among remaining ones of the plurality of nucleic acid base sequences which shares a fixed length sequence ~~has a second fixed-length partial sequence exactly matching with a first partial sequence of said first consensus sequence with reference to said table~~;

determining if the consensus sequence and the second nucleic acid base sequence can be assembled by comparing the consensus and the second sequence where they are aligned at the exactly matching fixed length sequence ~~a sequence adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence searched in said searching step with a sequence adjacent to said first fixed-length partial sequence of said first consensus sequence to be sufficiently similar via a high speed algorithm thereby determining the second nucleic acid base sequence can be assembled to said first consensus sequence~~; and if similar

assembling said consensus sequence and second nucleic acid base sequences ~~to said first consensus sequence so as~~ to reconstruct a ~~reconstructed first~~ new consensus sequence to repeatedly carry out the searching and determination steps. ~~if the second nucleic acid base sequence is determined to be assembled to the first consensus sequence.~~

4.   (Previously Presented) The method for assembling nucleic acid base sequences according to claim 3, wherein a sequence whose base length is the longest among the plurality of nucleic acid base sequences is selected as said first nucleic acid base sequence.

5.   (Currently Amended) A method for assembling nucleic acid base sequences comprising:

a first step of sorting a plurality of nucleic acid base sequences in descending order of sequence lengths;

a second step of entering, <u>into a table,</u> identification information of each of the plurality of nucleic acid base sequences and a respective pair of fixed <u>base</u> length partial sequences located in a terminal region thereof;

a third step of selecting one of the nucleic acid base sequences whose sequence length is the longest among the plurality of nucleic acid base sequences as a first consensus sequence;

a fourth step of moving a fixed <u>base</u> length <u>alignment</u> window along said consensus sequence to define a first fixed-length partial sequence and simultaneously searching for a second nucleic acid base sequence among remaining ones of the plurality of nucleic acid base sequences which has <u>an exact match with the fixed base length alignment window</u> ~~a second fixed-length partial sequence exactly matching with the first fixed-length partial sequence defined by said fixed-length window with reference to said table~~;

a fifth step of <u>determining if the consensus sequence and the second sequence can be assembled by</u> comparing <u>the consensus sequence and the seond sequence where they are aligned at the exactly matching fixed-length partial sequence</u> ~~a sequence adjacent to said first fixed-length partial sequence of said first consensus sequence with a sequence adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence searched in said fourth step to be sufficiently similar via a high-speed algorithm thereby determining said first consensus sequence and the second nucleic acid base sequence to be assembled; and~~

a sixth step of assembling the ~~first~~ consensus and second partial sequences to reconstruct a new consensus sequence ~~second nucleic acid base sequence searched in said fourth step to said first consensus sequence so as to reconstruct a reconstructed first consensus sequence if said fifth step determines that the sequences are to be assembled,~~

wherein the fourth step to the sixth step are repeated until said fixed <u>base</u> length <u>alignment</u> window completes the scanning throughout said reconstructed ~~first~~ consensus sequence, and said third step to said sixth step are repeated until all of the plurality of nucleic acid base sequences are selected in the <u>third or</u> fourth step and compared in the fifth step.

6.   (Previously Presented) The method for assembling nucleic acid base sequences according to claim 3, further comprising a step of picking up more than two of said

5

fixed-length partial sequences to be entered into said table for each of the plurality of nucleic acid base sequences.

7.   (Currently amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising the [[a]] step of designating a range of the terminal region of said ~~first~~ nucleic acid base sequence from which said fixed base length partial sequences to be entered into said table is extracted.

8.   (Currently amended) The method for assembling nucleic acid base sequences according to claim 3, wherein the [[a]] base length of said fixed base length partial sequences to be entered into said table is between 10 bases ~~and~~ to 32 bases.

9.   (Currently amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising the steps of:

    ~~a step of~~ specifying an upper limit c as an expected number of entries retrieved from said table of a ~~of an identical~~ fixed base length partial sequence located in different nucleic acid base sequences or different positions in the plurality of nucleic acid base ~~to be assembled to said first consensus~~ sequences, and

    ~~a step of~~ specifying a length s of fixed base length sequences to be entered into said table as an integer satisfying the following expression (1)

$$s \geq \frac{1}{2} \log \frac{KN}{c} \quad \cdots (1)$$

    where N is the number of said plurality of nucleic acid base sequences and K is the number of the fixed base length sequences selected from each of the plurality of nucleic acid base sequences.

10.   (Cancelled)

11.   (Currently amended) The method for assembling nucleic acid base sequences according to claim 3, wherein each of said fixed base length sequences is represented by a fixed number of computing words which are independent [[of a]] of the length of the fixed-length partial sequences.

12.   (Previously Presented) The method for assembling nucleic acid base sequences

according to claim 3, wherein any entry in said table is removed if a number of entries sharing an identical key therein is more than a previously specified number.

13-15. (Cancelled)

16. (New) The method of claim 1, wherein a greedy algorithm is used to compare the similarity between the sequence adjacent to the aligned window of said first nucleic acid base sequence with a sequence adjacent to the aligned window of said second nucleic acid base sequence.

17. (New). The method of claim 3, wherein a greedy algorithm is used to compare the consensus and the second sequence.

18. (New) The method of claim 5, wherein a greedy algorithm is used to compare the consensus and the second sequence.